

SEQUENCE LISTING

<110> ALBANI, SALVATORE

<120> METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION
AND MODULATION OF ANTIGEN-SPECIFIC T CELLS

<130> AND-TCCCIPI1-DIV2

<140>

<141>

<150> 09/756,983

<151> 2001-01-09

<150> PCT/US99/24666

<151> 1999-10-19

<150> 09/421,506

<151> 1999-10-19

<150> 60/105,018

<151> 1998-10-20

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived
from third hyper V region of IE molecule of Mus musculus

<400> 1

Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys
1 5 10 15

Ala

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide derived
from bole I protein of Epstein Barr virus

<400> 2

Thr Arg Asp Asp Ala Glu Tyr Leu Leu Gly Arg Glu Ser Val Leu
1 5 10 15

<210> 3
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide derived from the haemophilus influenza virus

<400> 3
Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys
1 5 10 15

<210> 4
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide derived from the TCR receptor of Mus musculus

<220>
<221> MOD_RES
<222> (18)
<223> Ser, Ile or Thr

<400> 4
Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys
1 5 10 15

Ala Xaa Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro
20 25 30

Gly Thr Arg Leu
35

<210> 5
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide derived from the influenza virus

<400> 5
Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

<210> 6
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide derived
from the influenza virus

<400> 6
Val Lys Leu Gly Glu Phe Tyr Asn Gln
1 5

<210> 7
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (2)
<223> cyclohexylalanine

<400> 7
Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala
1 5 10

<210> 8
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide derived
from the influenza virus

<400> 8
Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 9
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial

<400> 9
Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
1 5 10 15

Arg

<210> 10

<211> 15

<212> PRT

<213> Escherichia coli

<400> 10

Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu
1 5 10 15

<210> 11

<211> 15

<212> PRT

<213> Homo sapiens

<400> 11

Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly
1 5 10 15

<210> 12

<211> 9

<212> PRT

<213> Homo sapiens

<400> 12

Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

<210> 13

<211> 9

<212> PRT

<213> Homo sapiens

<400> 13

Val Lys Leu Gly Glu Phe Tyr Asn Gln
1 5

<210> 14

<211> 13

<212> PRT

<213> Homo sapiens

<400> 14

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

<210> 15

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<220>
 <221> CDS
 <222> (1)..(939)

<400> 15 atg ggc cac aca cgg agg cag gga aca tca cca tcc aag tgt cca tac Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr 1 5 10 15	48
ctc aat ttc ttt cag ctc ttg gtg ctg gct ggt ctt tct cac ttc tgt Leu Asn Phe Phe Gln Leu Leu Val Ala Gly Leu Ser His Phe Cys 20 25 30	96
tca ggt gtt atc cac gtg acc aag gaa gtg aaa gaa gtg gca acg ctg Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu 35 40 45	144
tcc tgt ggt cac aat gtt tct gtt gaa gag ctg gca caa act cgc atc Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile 50 55 60	192
tac tgg caa aag gag aag aaa atg gtg ctg act atg atg tct ggg gac Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp 65 70 75 80	240
atg aat ata tgg ccc gag tac aag aac cgg acc atc ttt gat atc act Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr 85 90 95	288
aat aac ctc tcc att gtg atc ctg gct ctg cgc cca tct gac gag ggc Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly 100 105 110	336
aca tac gag tgt gtt ctg aag tat gaa aaa gac gct ttc aag cgg Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg 115 120 125	384
gaa cac ctg gct gaa gtg acg tta tca gtc aaa gct gac ttc cct aca Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr 130 135 140	432
cct agt ata tct gac ttt gaa att cca act tct aat att aga agg ata Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile 145 150 155 160	480
att tgc tca acc tct gga ggt ttt cca gag cct cac ctc tcc tgg ttg Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu 165 170 175	528
gaa aat gga gaa gaa tta aat gcc atc aac aca aca gtt tcc caa gat Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp 180 185 190	576
cct gaa act gag ctc tat gct gtt agc gaa ttc ggc ggc tcc ggt ggt Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly 195 200 205	624

agc gcc aca cct caa aat att act gat ttg tgt gca gaa tac cac aac	672
Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn	
210	215
	220
aca caa ata cat acg cta aat gat aag ata ttt tcg tat aca gaa tct	720
Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser	
225	230
	235
	240
cta gct gga aaa aga gag atg gct atc att act ttt aag aat ggt gca	768
Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala	
245	250
	255
act ttt caa gta gaa gta cca ggt agt caa cat ata gat tca caa aaa	816
Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys	
260	265
	270
aaa gcg att gaa agg atg aag gat acc ctg agg att gca tat ctt act	864
Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr	
275	280
	285
gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa acg cct cat	912
Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His	
290	295
	300
gcg att gcc gca att agt atg gca aat taa	942
Ala Ile Ala Ala Ile Ser Met Ala Asn	
305	310

<210> 16
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<400> 16			
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr			
1	5	10	15
Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys			
20	25	30	
Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu			
35	40	45	
Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile			
50	55	60	
Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp			
65	70	75	80
Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr			
85	90	95	

Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	Pro	Ser	Asp	Glu	Gly
100							105							110	
Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	Asp	Ala	Phe	Lys	Arg
115						120								125	
Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	Ala	Asp	Phe	Pro	Thr
130						135								140	
Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	Asn	Ile	Arg	Arg	Ile
145						150								155	
Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	Leu	Ser	Trp	Leu
														175	
165									170						
Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	Val	Ser	Gln	Asp
									185					190	
180															
Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Glu	Phe	Gly	Gly	Ser	Gly	Gly
														205	
195							200								
Ser	Ala	Thr	Pro	Gln	Asn	Ile	Thr	Asp	Leu	Cys	Ala	Glu	Tyr	His	Asn
														220	
210						215									
Thr	Gln	Ile	His	Thr	Leu	Asn	Asp	Lys	Ile	Phe	Ser	Tyr	Thr	Glu	Ser
														240	
225						230									
Leu	Ala	Gly	Lys	Arg	Glu	Met	Ala	Ile	Ile	Thr	Phe	Lys	Asn	Gly	Ala
														255	
245									250						
Thr	Phe	Gln	Val	Glu	Val	Pro	Gly	Ser	Gln	His	Ile	Asp	Ser	Gln	Lys
														270	
260								265							
Lys	Ala	Ile	Glu	Arg	Met	Lys	Asp	Thr	Leu	Arg	Ile	Ala	Tyr	Leu	Thr
														285	
275							280								
Glu	Ala	Lys	Val	Glu	Lys	Leu	Cys	Val	Trp	Asn	Asn	Lys	Thr	Pro	His
														300	
290						295									
Ala	Ile	Ala	Ala	Ile	Ser	Met	Ala	Asn							
						310									

<210> 17
<211> 1056
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<220>
<221> CDS
<222> (1)..(1053)

<400> 17
 atg gga ctg agt aac att ctc ttt gtg atg gcc ttc ctg ctc tct ggt 48
 Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
 1 5 10 15

 gct gct cct ctg aag att caa gct tat ttc aat gag act gca gac ctg 96
 Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
 20 25 30

 cca tgc caa ttt gca aac tct caa aac caa agc ctg agt gag cta gta 144
 Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
 35 40 45

 gta ttt tgg cag gac cag gaa aac ttg gtt ctg aat gag gta tac tta 192
 Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
 50 55 60

 ggc aaa gag aaa ttt gac agt gtt cat tcc aag tat atg ggc cgc aca 240
 Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
 65 70 75 80

 agt ttt gat tcg gac agt tgg acc ctg aga ctt cac aat ctt cag atc 288
 Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
 85 90 95

 aag gac aag ggc ttg tat caa tgt atc atc cat cac aaa aag ccc aca 336
 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
 100 105 110

 gga atg att cgc atc cac cag atg aat tct gaa ctg tca gtg ctt gct 384
 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
 115 120 125

 aac ttc agt caa cct gaa ata gta cca att tct aat ata aca gaa aat 432
 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
 130 135 140

 gtg tac ata aat ttg acc tgc tca tct ata cac ggt tac cca gaa cct 480
 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
 145 150 155 160

 aag aag atg agt gtt ttg cta aga acc aag aat tca act atc gag tat 528
 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
 165 170 175

 gat ggt att atg cag aaa tct caa gat aat gtc aca gaa ctg tac gac 576
 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
 180 185 190

 gtt tcc atc agc ttg tct gtt tca ttc cct gat gtt acg agc aat atg 624
 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
 195 200 205

 acc atc ttc tgt att ctg gaa act gac aag acg cgg ctt tta tct tca 672
 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
 210 215 220

cct ttc tct ata gag ctt gag gac cct cag cct ccc cca gac cac gaa	720
Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu	
225 230 235 240	
ttc ggc ggc tcc ggt ggt agc gcc aca cct caa aat att act gat ttg	768
Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu	
245 250 255	
tgt gca gaa tac cac aac aca caa ata cat acg cta aat gat aag ata	816
Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile	
260 265 270	
ttt tcg tat aca gaa tct cta gct gga aaa aga gag atg gct atc att	864
Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile	
275 280 285	
act ttt aag aat ggt gca act ttt caa gta gaa gta cca ggt agt caa	912
Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln	
290 295 300	
cat ata gat tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg	960
His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu	
305 310 315 320	
agg att gca tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg	1008
Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp	
325 330 335	
aat aat aaa acg cct cat gcg att gcc gca att agt atg gca aat taa	1056
Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn	
340 345 350	

<210> 18

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<400> 18

Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
1 5 10 15Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
20 25 30Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
35 40 45Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
50 55 60Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
65 70 75 80

Ser Phe Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
 85 90 95
 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
 100 105 110
 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
 115 120 125
 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
 130 135 140
 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
 145 150 155 160
 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
 165 170 175
 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
 180 185 190
 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
 195 200 205
 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
 210 215 220
 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu
 225 230 235 240
 Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu
 245 250 255
 Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile
 260 265 270
 Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile
 275 280 285
 Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln
 290 295 300
 His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu
 305 310 315 320
 Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp
 325 330 335
 Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 340 345 350

<210> 19
<211> 31
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 19

Ser Ala Gln Leu Glu Trp Glu Leu Gln Ala	Leu Glu Lys Glu Asn Ala
1	5
10	15

Gln Leu Glu Trp Glu Leu Gln Ala	Leu Glu Lys Glu Leu Ala Gln
20	25
30	

<210> 20

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 20

Ala Gln Leu Lys Lys Leu Gln Ala	Leu Lys Lys Lys Asn Ala Gln
1	5
10	15

Leu Lys Gln Lys Leu Gln Ala	Leu Lys Lys Lys Leu Ala Gln
20	25
30	

<210> 21

<211> 1095

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<220>

<221> CDS

<222> (1)..(1092)

<400> 21

atg gcc ata agt gga gtc cct gtg cta gga ttt ttc atc ata gct gtg	48
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val	
1	5
10	15

ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc	96
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile	
20	25
30	

atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg	144
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met	
35	40
45	

ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag	192
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys	
50	55
60	

gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag		240	
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu			
65	70	75	80
gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ctg gaa		288	
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu			
85	90	95	
atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca		336	
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro			
100	105	110	
gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac		384	
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn			
115	120	125	
gtc ctc atc tgt ttc atc gac aag ttc acc cca cca gtg gtc aat gtc		432	
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val			
130	135	140	
acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca		480	
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr			
145	150	155	160
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc		528	
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu			
165	170	175	
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac		576	
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His			
180	185	190	
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca		624	
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro			
195	200	205	
agc cct ctc cca gag act aca gag gaa ttc ggt ggt tcc ggt ggt tcc		672	
Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser			
210	215	220	
gcg cag ctg gaa tgg gaa ctg cag gcg ctg gaa aaa gaa aac gcg cag		720	
Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln			
225	230	235	240
ctg gaa tgg gaa ctg cag gcg ctg gaa aaa gaa ctg gcg cag ggc ggc		768	
Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly			
245	250	255	
tcc ggt ggt agc gcc aca cct caa aat att act gat ttg tgt gca gaa		816	
Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu			
260	265	270	
tac cac aac aca caa ata cat acg cta aat gat aag ata ttt tcg tat		864	
Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr			
275	280	285	

aca gaa tct cta gct gga aaa aga gag atg gct atc att act ttt aag	912
Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys	
290	295
	300
aat ggt gca act ttt caa gta gaa gta cca ggt agt caa cat ata gat	960
Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp	
305	310
	315
	320
tca caa aaa aaa gcg att gaa agg atg aag gat acc ctg agg att gca	1008
Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala	
325	330
	335
tat ctt act gaa gct aaa gtc gaa aag tta tgt gta tgg aat aat aaa	1056
Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys	
340	345
	350
acg cct cat gcg att gcc gca att agt atg gca aat taa	1095
Thr Pro His Ala Ile Ala Ile Ser Met Ala Asn	
355	360

<210> 22

<211> 364

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<400> 22

Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
1 5 10 15Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
20 25 30Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
35 40 45Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
50 55 60Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
65 70 75 80Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
85 90 95Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
100 105 110Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
115 120 125Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
 165 170 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
 180 185 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
 195 200 205

Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser
 210 215 220

Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln
 225 230 235 240

Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly
 245 250 255

Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu
 260 265 270

Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr
 275 280 285

Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
 290 295 300

Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
 305 310 315 320

Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
 325 330 335

Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
 340 345 350

Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 355 360

<210> 23
 <211> 861
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct with
 human and bacterial sequences

<220>
 <221> CDS
 <222> (1)...(855)

<400> 23				
atg gtg tgt ctg aag ttc cct gga ggc tcc tgc atg gca gct ctg aca	48			
Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr				
1 5 10 15				
gtg aca ctg atg gtg ctg agc tcc cca ctg gct ttg gct ggg gac acc	96			
Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr				
20 25 30				
cga cca cgt ttc ttg gag cag gtt aaa cat gag tgt cat ttc ttc aac	144			
Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn				
35 40 45				
ggg acg gag cgg gtg cgg ttc ctg gac aga tac ttc tat cac caa gag	192			
Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu				
50 55 60				
gag tac gtg cgc ttc gac agc gac gtg ggg gag tac cgg gcg gtg acg	240			
Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr				
65 70 75 80				
gag ctg ggg cgg cct gat gcc gag tac tgg aac agc cag aag gac ctc	288			
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu				
85 90 95				
ctg gag cag aag cgg gcc gcg gtg gac acc tac tgc aga cac aac tac	336			
Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr				
100 105 110				
ggg gtt ggt gag agc ttc aca gtg cag cgg cga gtc tat cct gag gtg	384			
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val				
115 120 125				
act gtg tat cct gca aag acc cag ccc ctg cag cac cac aac ctc ctg	432			
Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu				
130 135 140				
gtc tgc tct gtg aat ggt ttc tat cca ggc agc att gaa gtc agg tgg	480			
Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp				
145 150 155 160				
tcc cgg aac ggc cag gaa gag aag act ggg gtg gtg tcc aca ggc ctg	528			
Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu				
165 170 175				
atc cag aat gga gac tgg acc ttc cag acc ctg gtg atg ctg gaa aca	576			
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr				
180 185 190				
gtt cct cgg agt gga gag gtt tac acc tgc caa gtg gag cac cca agc	624			
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser				
195 200 205				
ctg acg agc cct ctc aca gtg gaa tgg aga gca cgg tct gaa tct gca	672			
Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala				
210 215 220				

cag agc aag ggc ggc tcc ggt ggt agc gcc cag ctg aag aag aaa ctc		720
Gln Ser Lys Gly Gly Ser Gly Ser Ala Gln Leu Lys Lys Lys Leu		
225	230	235
240		
cag gct ctg aaa aaa aag aat gcc cag ctc aag cag aag ctg cag gcc		768
Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala		
245	250	255
ctg aag aaa aag ctg gct cag ggt tcc ggt ggt tcc gcg ggt ggt ggt		816
Leu Lys Lys Leu Ala Gln Gly Ser Gly Ser Ala Gly Gly Gly		
260	265	270
ttg aac gac atc ttc gaa gct cag aaa atc gaa tgg cac taataa		861
Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His		
275	280	285

<210> 24
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion construct with
human and bacterial sequences

<400> 24			
Met Val Cys Leu Lys Phe Pro Gly Gly Ser Cys Met Ala Ala Leu Thr			
1	5	10	15
Val Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr			
20	25	30	
Arg Pro Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn			
35	40	45	
Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu			
50	55	60	
Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr			
65	70	75	80
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu			
85	90	95	
Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr			
100	105	110	
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val			
115	120	125	
Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu			
130	135	140	
Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp			
145	150	155	160

Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu
165 170 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr
180 185 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
195 200 205

Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
210 215 220

Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
225 230 235 240

Gln Ala Leu Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
245 250 255

Leu Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
260 265 270

Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
275 280 285